

SEQUENCE LISTING



<110> AMANO ENZYME INC.
Takeuchi, Ken-Ichi
Isobe, Kimiyasu
Moriguchi, Mitsuaki
Hirose, Yoshihiko
Koide, Yoshinao

<120> TRANSFORMED MICROORGANISM AND PROCESS FOR PRODUCING D-AMINOACYLASE

<130> 217301US-0

<140> 10/009,782

<141> 2002-03-25

<150> PCT/JP00/03932

<151> 2000-06-15

<150> JAPAN 11/170555

<151> 1999-06-17

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<170> PatentIn version 3.1

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<213> Alcaligenes xylosoxydans subsp. xylosoxydans

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<221> CDS

<222> (34)..(1485)

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Pro	Phe	Asp	Leu	Leu	Leu	Ala	Gly	Gly	Thr	Leu	Ile	Asp	Gly	Ser	Asn	
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acc	ccg	ggg	cgg	cgc	gcc	gac	ctg	ggc	gtg	cgc	ggc	gac	cgc	atc	gcc	150
Thr	Pro	Gly	Arg	Arg	Ala	Asp	Leu	Gly	Val	Arg	Gly	Asp	Arg	Ile	Ala	
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gcc	atc	ggc	gat	ctg	tcg	gac	gcc	gcc	gcg	cac	acc	cgg	gtc	gac	gtg	198
Ala	Ile	Gly	Asp	Leu	Ser	Asp	Ala	Ala	Ala	His	Thr	Arg	Val	Asp	Val	
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tcg	ggc	ctg	gtg	gtc	gcg	ccc	ggc	ttc	atc	gac	tcg	cac	acc	cac	gac	246
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Asp	Asn	Tyr	Leu	Leu	Arg	Arg	Arg	Asp	Met	Thr	Pro	Lys	Ile	Ser	Gln	
			75					80					85			
ggc	gtc	acc	acg	gtg	gtc	acg	ggc	aat	tgc	ggc	atc	agc	ctg	gcg	ccg	342
Gly	Val	Thr	Thr	Val	Val	Thr	Gly	Asn	Cys	Gly	Ile	Ser	Leu	Ala	Pro	
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ctg	gcg	cac	gcc	aac	ccg	ccc	gcc	ccc	ctg	gac	ctg	ctg	gac	gaa	ggc	390
Leu	Ala	His	Ala	Asn	Pro	Pro	Ala	Pro	Leu	Asp	Leu	Leu	Asp	Glu	Gly	
	105					110					115					
ggc	tct	tac	cgt	ttc	gag	cgc	ttc	gcc	gac	tac	ctg	gac	gcg	ttg	cgg	438
Gly	Ser	Tyr	Arg	Phe	Glu	Arg	Phe	Ala	Asp	Tyr	Leu	Asp	Ala	Leu	Arg	
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Ala	Thr	Pro	Ala	Ala	Val	Asn	Ala	Ala	Cys	Met	Val	Gly	His	Ser	Thr	
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ctg	cgc	gcc	gcg	gtc	atg	ccg	gac	ttg	cag	cgc	gcc	gcc	acc	gac	gag	534
Leu	Arg	Ala	Ala	Val	Met	Pro	Asp	Leu	Gln	Arg	Ala	Ala	Thr	Asp	Glu	
			155					160					165			
gaa	atc	gcg	gcc	atg	cgg	gac	ctg	gcc	gag	gaa	gcc	atg	gcc	agc	ggc	582
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Ala	Ile	Gly	Ile	Ser	Thr	Gly	Ala	Phe	Tyr	Pro	Pro	Ala	Ala	Arg	Ala	
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Gly	Ile	Tyr	Ala	Thr	His	Met	Arg	Asp	Glu	Gly	Glu	His	Ile	Val	Ala	
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Ala	Leu	Glu	Glu	Thr	Phe	Arg	Ile	Gly	Arg	Glu	Leu	Asp	Val	Pro	Val	
			235					240					245			
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cgc	gag	acg	ctg	ccg	ctg	atc	gag	gcc	gcc	atg	gcg	cgc	cag	gac	gtc	870

Arg	Glu	Thr	Leu	Pro	Leu	Ile	Glu	Ala	Ala	Met	Ala	Arg	Gln	Asp	Val	
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Asp	Arg	Val	Leu	Leu	Ala	Gly	Arg	Thr	Ile	Ile	Thr	Trp	Cys	Lys	Pro	
				300					305					310		
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Phe	Pro	Glu	Leu	Ser	Gly	Arg	Asp	Leu	Asp	Glu	Val	Ala	Ala	Glu	Arg	
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Ile	Tyr	Phe	Met	Met	Asp	Glu	Pro	Asp	Val	Gln	Arg	Ile	Leu	Ala	Phe	
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cat	ccg	cgc	ctg	tgg	ggc	acc	ttc	ccg	cgg	gtg	ctg	ggg	cac	tat	gcg	1206
His	Pro	Arg	Leu	Trp	Gly	Thr	Phe	Pro	Arg	Val	Leu	Gly	His	Tyr	Ala	
				380					385					390		
cgc	gac	ctg	ggc	ctg	ttc	ccg	ctg	gag	acg	gcg	gta	tgg	aag	atg	acc	1254
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			395					400					405			
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Gly	Leu	Thr	Ala	Ala	Arg	Phe	Gly	Leu	Ala	Gly	Arg	Gly	Gln	Leu	Gln	
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Ala	Gly	Tyr	Phe	Ala	Asp	Leu	Val	Val	Phe	Asp	Pro	Ala	Thr	Val	Ala	
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gat	acc	gcc	acc	ttc	gaa	cac	cct	acc	gag	cgc	gcc	gcc	ggc	atc	cat	1398
Asp	Thr	Ala	Thr	Phe	Glu	His	Pro	Thr	Glu	Arg	Ala	Ala	Gly	Ile	His	
440					445					450					455	
tcc	gtg	tac	gtc	aac	ggc	gcg	ccg	gtc	tgg	caa	gag	cag	gcg	ttc	acc	1446
Ser	Val	Tyr	Val	Asn	Gly	Ala	Pro	Val	Trp	Gln	Glu	Gln	Ala	Phe	Thr	
				460					465					470		
ggc	cag	cat	gcc	ggc	cgc	gtg	ctc	gca	cgc	acg	gcc	gcc	tgag	cccc	ggc	1495

Gly Gln His Ala Gly Arg Val Leu Ala Arg Thr Ala Ala
 475 480

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Val Arg Gly Asp Arg Ile Ala Ala Ile Gly Asp Leu Ser Asp Ala Ala
 35 40 45

Ala His Thr Arg Val Asp Val Ser Gly Leu Val Val Ala Pro Gly Phe
 50 55 60

Ile Asp Ser His Thr His Asp Asp Asn Tyr Leu Leu Arg Arg Arg Asp
 65 70 75 80

Met Thr Pro Lys Ile Ser Gln Gly Val Thr Thr Val Val Thr Gly Asn
 85 90 95

Cys Gly Ile Ser Leu Ala Pro Leu Ala His Ala Asn Pro Pro Ala Pro
 100 105 110

Leu Asp Leu Leu Asp Glu Gly Gly Ser Tyr Arg Phe Glu Arg Phe Ala
 115 120 125

Asp Tyr Leu Asp Ala Leu Arg Ala Thr Pro Ala Ala Val Asn Ala Ala
130 135 140

Cys Met Val Gly His Ser Thr Leu Arg Ala Ala Val Met Pro Asp Leu
145 150 155 160

Gln Arg Ala Ala Thr Asp Glu Glu Ile Ala Ala Met Arg Asp Leu Ala
165 170 175

Glu Glu Ala Met Ala Ser Gly Ala Ile Gly Ile Ser Thr Gly Ala Phe
180 185 190

Tyr Pro Pro Ala Ala Arg Ala Thr Thr Glu Glu Ile Ile Glu Val Cys
195 200 205

Arg Pro Leu Ser Ala His Gly Gly Ile Tyr Ala Thr His Met Arg Asp
210 215 220

Glu Gly Glu His Ile Val Ala Ala Leu Glu Glu Thr Phe Arg Ile Gly
225 230 235 240

Arg Glu Leu Asp Val Pro Val Val Ile Ser His His Lys Val Met Gly
245 250 255

Gln Pro Asn Phe Gly Arg Ser Arg Glu Thr Leu Pro Leu Ile Glu Ala
260 265 270

Ala Met Ala Arg Gln Asp Val Ser Leu Asp Ala Tyr Pro Tyr Val Ala
275 280 285

Gly Ser Thr Met Leu Lys Gln Asp Arg Val Leu Leu Ala Gly Arg Thr
290 295 300

Ile Ile Thr Trp Cys Lys Pro Phe Pro Glu Leu Ser Gly Arg Asp Leu
305 310 315 320

Asp Glu Val Ala Ala Glu Arg Gly Lys Ser Lys Tyr Asp Val Val Pro
325 330 335

Glu Leu Gln Pro Ala Gly Ala Ile Tyr Phe Met Met Asp Glu Pro Asp
340 345 350

Val Gln Arg Ile Leu Ala Phe Gly Pro Thr Met Ile Gly Ser Asp Gly
355 360 365

Leu Pro His Asp Glu Arg Pro His Pro Arg Leu Trp Gly Thr Phe Pro
370 375 380

Arg Val Leu Gly His Tyr Ala Arg Asp Leu Gly Leu Phe Pro Leu Glu
385 390 395 400

Thr Ala Val Trp Lys Met Thr Gly Leu Thr Ala Ala Arg Phe Gly Leu
405 410 415

Ala Gly Arg Gly Gln Leu Gln Ala Gly Tyr Phe Ala Asp Leu Val Val
420 425 430

Phe Asp Pro Ala Thr Val Ala Asp Thr Ala Thr Phe Glu His Pro Thr
435 440 445

Glu Arg Ala Ala Gly Ile His Ser Val Tyr Val Asn Gly Ala Pro Val
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Trp Gln Glu Gln Ala Phe Thr Gly Gln His Ala Gly Arg Val Leu Ala
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Arg Thr Ala Ala

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<223> Nucleotide sequence in ribosome binding site for improving translation efficiency.

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